

REMARKS

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. §§1.821(e), (f) and (g), or §§1.825(d) and (b), respectively, are the same, and that the attached sequence listing and computer readable form copy contain no new matter. A copy of the "Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures" is also enclosed.

Applicant does not believe there are any fees required for the submission of this sequence listing. However, the Commissioner is authorized to charge Lyon & Lyon's Deposit Account No. 12-2475 for any fees required and to credit any overpayments to said Deposit Account 12-2475.

Respectfully submitted,

LYON & LYON LLP

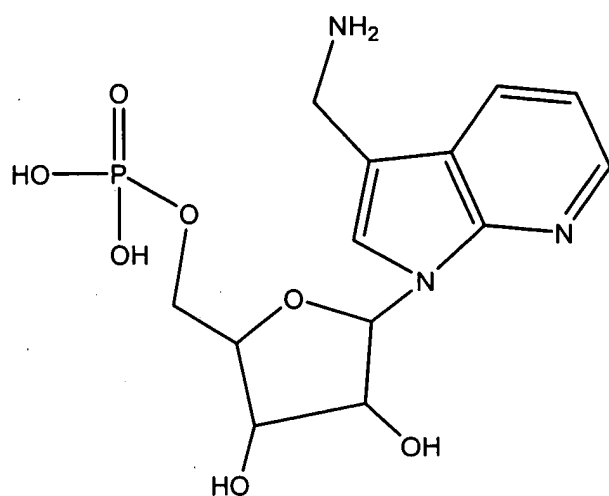
Dated: August 9, 2001

By: 

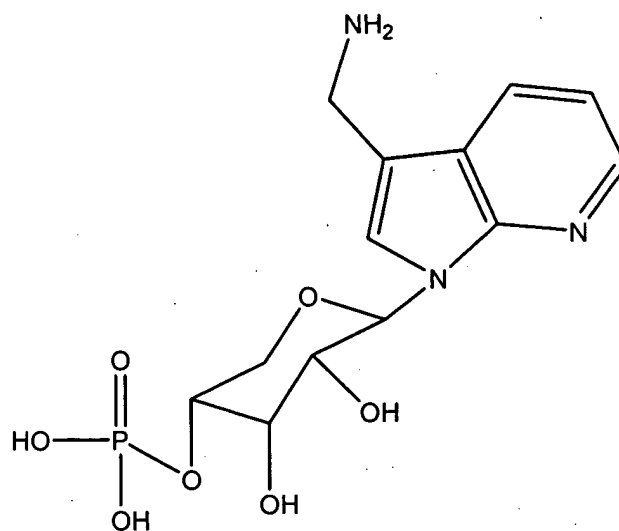
Patrick S. Eagleman
Reg. No. 44,665

633 West Fifth Street, Suite 4700
Los Angeles, California 90071-2066
(213) 489-1600

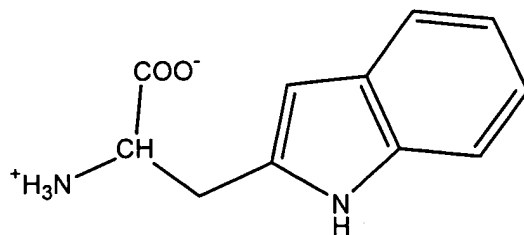
ILLUSTRATIONS



Tryptamine furanosyl nucleoside
(RNA)



Tryptamine pyranosyl nucleoside
(p-RNA)



Tryptophan
(Amino Acid)



UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office

Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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09/374,376 08/13/99 HELLER M 241/172

022249
LYON & LYON LLP
633 WEST FIFTH STREET
SUITE 4700
LOS ANGELES CA 90071

HM12/1001

EXAMINER

PRASTHOPE, J

ART UNIT	PAPER NUMBER
----------	--------------

1627

DATE MAILED: 10/01/01

*Att: DBM-α
P. Eagan-α*

*cc: RNS
LWD
Hema*

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trad marks

RECEIVED
OCT 04 2001
U.S. PROSECUTION

Notice of Abandonment

Application No.

09/374,338

Examiner

Thomas W Prasthofer

Applicant(s)

HELLER ET AL.

Art Unit

1627

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address--

This application is abandoned in view of:

1. ☒ Applicant's failure to timely file a proper reply to the Office letter mailed on 24 July 2001.

(a) ☐ A reply was received on _____ (with a Certificate of Mailing or Transmission dated _____), which is after the expiration of the period for reply (including a total extension of time of _____ month(s)) which expired on _____.

(b) ☐ A proposed reply was received on _____, but it does not constitute a proper reply under 37 CFR 1.113 (a) to the final rejection.

(A proper reply under 37 CFR 1.113 to a final rejection consists only of: (1) a timely filed amendment which places the application in condition for allowance; (2) a timely filed Notice of Appeal (with appeal fee); or (3) a timely filed Request for Continued Examination (RCE) in compliance with 37 CFR 1.114).

(c) ☐ No reply has been received.

2. ☐ Applicant's failure to timely pay the required issue fee and publication fee, if applicable, within the statutory period of three months from the mailing date of the Notice of Allowance (PTOL-85).

(a) ☐ The issue fee and publication fee, if applicable, was received on _____ (with a Certificate of Mailing or Transmission dated _____), which is after the expiration of the statutory period for payment of the issue fee (and publication fee) set in the Notice of Allowance.

(b) ☐ The submitted fee of \$_____ is insufficient. A balance of \$_____ is due.

The issue fee required by 37 CFR 1.18 is \$_____. The publication fee, if required by 37 CFR 1.18(d), is \$_____.

(c) ☐ The issue fee and publication fee, if applicable, has not been received.

3. ☐ Applicant's failure to timely file new formal drawings as required by, and within the three-month period set in, the Notice of Allowability (PTO-37):

(a) ☐ Proposed new formal drawings were received on _____ (with a Certificate of Mailing or Transmission dated _____), which is after the expiration of the period for reply.

(b) ☐ The proposed new formal drawings filed on _____ are not acceptable and the period for reply has expired.

(c) ☐ No proposed new formal drawings have been received.


4. ☐ The letter of express abandonment which is signed by the attorney or agent of record, the assignee of the entire interest, or all of the applicants.

5. ☐ The letter of express abandonment which is signed by an attorney or agent (acting in a representative capacity under 37 CFR 1.34(a)) upon the filing of a continuing application.

6. ☐ The decision by the Board of Patent Appeals and Interference rendered on _____ and because the period for seeking court review of the decision has expired and there are no allowed claims.

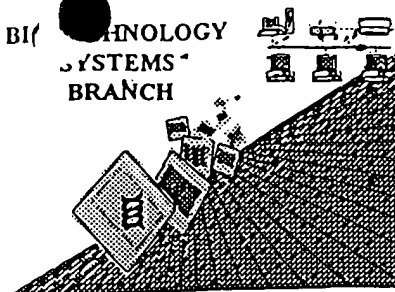
7. ☒ The reason(s) below:

Applicant's response to the communication mailed July 24, 2001 (Non-Bona Fide attempt to comply with the sequence rules) did not comply with the sequence rules, 37 C.F.R. 1.136. The application is abandoned under 37 C.F.R. 1.821(g). A copy of the sequence listing error report is attached.


DR. JYOTSNA VENKAT PH.D.
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

T. PRAST OFER

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/374 338 B

Source: CIPE

Date Processed by STIC: 08/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin31help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/374 338 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ✓ Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/374,338B

DATE: 08/23/2001
TIME: 13:24:31

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Heller, Michael J.
4 Windhab, Norbert
5 Anderson, Richard R.
6 Ackley, Donald E.
7 Nova, Tina S.
8 Hoppe, Hans-Ullrich
9 Hamon, Christian
11 <120> TITLE OF INVENTION: MICROELECTRONIC MOLECULAR DESCRIPTOR ARRAY DEVICES, METHODS,
PROCEDURES,
12 AND FORMATS FOR COMBINATORIAL SELECTION OF INTERMOLECULAR LIGAND BINDING
13 STRUCTURES AND FOR DRUG SCREENING
15 <130> FILE REFERENCE: Patrick Eagleman: Nanogen 241/172
17 <140> CURRENT APPLICATION NUMBER: 09/374,338B
18 <141> CURRENT FILING DATE: 1999-08-13
20 <160> NUMBER OF SEQ ID NOS: 31
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 7
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Synthetic test construct
32 <220> FEATURE:
33 <221> NAME/KEY: modified_base
34 <222> LOCATION: (1)..(7)
35 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
38 <220> FEATURE:
39 <221> NAME/KEY: modified_base
40 <222> LOCATION: (1)..(1)
41 <223> OTHER INFORMATION: Base 1 is tryptamine
44 <220> FEATURE:
45 <221> NAME/KEY: modified_base
46 <222> LOCATION: (7)..(7)
47 <223> OTHER INFORMATION: Base 7 is modified with Texas Red
50 <400> SEQUENCE: 1
W--> 51 ngaaggg
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 14
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Synthetic test construct
62 <220> FEATURE:
63 <221> NAME/KEY: modified_base
64 <222> LOCATION: (1)..(14)
65 <223> OTHER INFORMATION: Entire sequence is Pyranosyl
68 <220> FEATURE:
69 <221> NAME/KEY: modified_base

n can only represent a
single nucleotide base at any
single location.

FYI - tryptamine is an
amino acid or protein

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/374,338B

DATE: 08/23/2001
TIME: 13:24:31

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

70 <222> LOCATION: (1)..(1)
71 <223> OTHER INFORMATION: Base 1 is modified with Biotin
74 <220> FEATURE:
75 <221> NAME/KEY: modified_base
76 <222> LOCATION: (8)..(8)
77 <223> OTHER INFORMATION: Base 8 is tryptamine
80 <400> SEQUENCE: 2
W--> 81 cccttctncc cccg
84 <210> SEQ ID NO: 3
85 <211> LENGTH: 7
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
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90 <223> OTHER INFORMATION: Synthetic test construct
93 <220> FEATURE:
94 <221> NAME/KEY: modified_base
95 <222> LOCATION: (1)..(7)
96 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
99 <220> FEATURE:
100 <221> NAME/KEY: modified_base
101 <222> LOCATION: (1)..(1)
102 <223> OTHER INFORMATION: Base 1 is modified with Cyanine-3 fluorescent dye
105 <220> FEATURE:
106 <221> NAME/KEY: modified_base
107 <222> LOCATION: (7)..(7)
108 <223> OTHER INFORMATION: Base 7 is tryptamine
111 <400> SEQUENCE: 3
W--> 112 cgggggn Error
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 7
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Synthetic test construct
124 <220> FEATURE:
125 <221> NAME/KEY: modified_base
126 <222> LOCATION: (1)..(7)
127 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
130 <220> FEATURE:
131 <221> NAME/KEY: modified_base
132 <222> LOCATION: (3)..(3)
133 <223> OTHER INFORMATION: Base 3 is tryptamine
136 <220> FEATURE:
137 <221> NAME/KEY: modified_base
138 <222> LOCATION: (4)..(4)
139 <223> OTHER INFORMATION: Base 4 is tryptamine
142 <220> FEATURE:
143 <221> NAME/KEY: modified_base
144 <222> LOCATION: (5)..(5)

n can only represent a
single nucleotide base at
any single location.

n can only represent a
single nucleotide base at
any single location

FYI tryptamine is an
amino acid

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/374,338B

DATE: 08/23/2001
TIME: 13:24:31

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

145 <223> OTHER INFORMATION: Base 5 is tryptamine
148 <400> SEQUENCE: 4
W--> 149 ccnnngg 7
152 <210> SEQ ID NO: 5
153 <211> LENGTH: 7
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Synthetic test construct
161 <220> FEATURE:
162 <221> NAME/KEY: modified_base
163 <222> LOCATION: (1)..(7)
164 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
167 <220> FEATURE:
168 <221> NAME/KEY: modified_base
169 <222> LOCATION: (1)..(1)
170 <223> OTHER INFORMATION: Base 1 modified with Fluorophore
173 <220> FEATURE:
174 <221> NAME/KEY: modified_base
175 <222> LOCATION: (7)..(7)
176 <223> OTHER INFORMATION: Base 7 modified with a Peptide
179 <220> FEATURE:
180 <221> NAME/KEY: modified_base
181 <222> LOCATION: (7)..(7) *Errored*
182 <223> OTHER INFORMATION: Base 7 is tryptamine
185 <400> SEQUENCE: 5
W--> 186 cggggggh 7
189 <210> SEQ ID NO: 6
190 <211> LENGTH: 8
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: Synthetic test construct
198 <220> FEATURE:
199 <221> NAME/KEY: modified_base
200 <222> LOCATION: (1)..(8)
201 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
204 <220> FEATURE:
205 <221> NAME/KEY: modified_base
206 <222> LOCATION: (1)..(1)
207 <223> OTHER INFORMATION: Base 1 modified with a Peptide
210 <220> FEATURE:
211 <221> NAME/KEY: modified_base
212 <222> LOCATION: (1)..(1) *Errored*
213 <223> OTHER INFORMATION: Base 1 is tryptamine
216 <220> FEATURE:
217 <221> NAME/KEY: modified_base
218 <222> LOCATION: (8)..(8)
219 <223> OTHER INFORMATION: Base 8 is any nucleotide *OK*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/374,338B

DATE: 08/23/2001
TIME: 13:24:31

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

222 <400> SEQUENCE: 6
W--> 223 ngaagggg 8
226 <210> SEQ ID NO: 7
227 <211> LENGTH: 14
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229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Synthetic test construct
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236 <221> NAME/KEY: modified_base
237 <222> LOCATION: (1)..(14)
238 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
241 <220> FEATURE:
242 <221> NAME/KEY: modified_base
243 <222> LOCATION: (1)..(1)
244 <223> OTHER INFORMATION: Base 1 modified with Biotin
247 <220> FEATURE:
248 <221> NAME/KEY: modified_base
249 <222> LOCATION: (7)..(7)
250 <223> OTHER INFORMATION: Base 7 is tryptamine
253 <220> FEATURE:
254 <221> NAME/KEY: modified_base
255 <222> LOCATION: (7)..(8)
256 <223> OTHER INFORMATION: Bases 7 and 8 are modified by Peptide connection.
259 <400> SEQUENCE: 7
W--> 260 cccttcttcc cccg 14
263 <210> SEQ ID NO: 8
264 <211> LENGTH: 6
265 <212> TYPE: PRT
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Synthetic test construct
272 <220> FEATURE:
273 <221> NAME/KEY: PEPTIDE
274 <222> LOCATION: (1)..(1)
275 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
278 <400> SEQUENCE: 8
280 Cys Leu Ser Leu Glu Gly
281 1 5
283 <210> SEQ ID NO: 9
284 <211> LENGTH: 6
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Synthetic test construct
292 <220> FEATURE:
293 <221> NAME/KEY: PEPTIDE
294 <222> LOCATION: (1)..(1)
295 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/374,338B

DATE: 08/23/2001
TIME: 13:24:31

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

298 <400> SEQUENCE: 9
300 Cys Ser Leu Glu Ser Gly
301 1 5
303 <210> SEQ ID NO: 10
304 <211> LENGTH: 6
305 <212> TYPE: PRT
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Synthetic test construct ✓
312 <220> FEATURE:
313 <221> NAME/KEY: PEPTIDE
314 <222> LOCATION: (1)..(1)
315 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
318 <400> SEQUENCE: 10
320 Cys Leu Leu Ser Glu Gly
321 1 5
323 <210> SEQ ID NO: 11
324 <211> LENGTH: 6
325 <212> TYPE: PRT
326 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: Synthetic test construct ✓
332 <220> FEATURE:
333 <221> NAME/KEY: PEPTIDE
334 <222> LOCATION: (1)..(1)
335 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
338 <400> SEQUENCE: 11
340 Cys Ser Arg Ser Arg Gly
341 1 5
343 <210> SEQ ID NO: 12
344 <211> LENGTH: 6
345 <212> TYPE: PRT
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349 <223> OTHER INFORMATION: Synthetic test construct
352 <220> FEATURE:
353 <221> NAME/KEY: PEPTIDE
354 <222> LOCATION: (1)..(1)
355 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
358 <400> SEQUENCE: 12
360 Cys Ser Arg His Arg Gly
361 1 5
363 <210> SEQ ID NO: 13
364 <211> LENGTH: 6
365 <212> TYPE: PRT
366 <213> ORGANISM: Artificial Sequence
368 <220> FEATURE:
369 <223> OTHER INFORMATION: Synthetic test construct
372 <220> FEATURE:

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/374,338B

DATE: 08/23/2001
TIME: 13:24:32

Input Set : A:\ES.txt
Output Set: N:\CRF3\08162001\I374338B.raw

L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
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L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31